

Sub B1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.
 Baker, Kevin
 Chuntharapai, Anan
 Gurney, Austin
 Kim, Kyung Jin
10 Wood, William

(ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

15 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
20 (D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

25 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

30 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 12-Jun-1998
(C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/049911

(B) FILING DATE: 18-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

5 (A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110P1

(ix) TELECOMMUNICATION INFORMATION:

10 (A) TELEPHONE: 650/225-5416

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
1 5 10 15

Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
20 25 30

Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Arg
35 40 45

30 His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
50 55 60

Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
65 70 75

Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
80 85 90

Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
5 95 100 105

Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
110 115 120

Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
10 125 130 135

Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
140 145 150

Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
15 155 160 165

Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
20 170 175 180

Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
25 185 190 195

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
200 205 210

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
215 220 225

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
230 235 240

Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
35 245 250 255

Ile Val Phe Val

259

(2) INFORMATION FOR SEQ ID NO:2:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

150 GCTGTGGAA CCTCTCCACG CGCACGAAC CAGCCAACGA TTTCTGATAG 50

ATTTTTGGGA GTTGACCAAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100

CGTTAGGGAA CTCTGGGAC AGAGCGCCCC GGCGGCCTGA TGGCCGAGGC 150

200

AGGGTGGCAG CCAGGACCCA GGACGGCGTC GGGAACCAT A CC ATG 195

Met

1

250 GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234

Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile

5

10

300 GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273

Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr

15

20

25

350 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312

Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala

35 30 35 40

CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351
 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
 45 50

5 CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390
 Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
 55 60 65

AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429
 10 Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
 70 75

AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA 468
 Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys
 15 80 85 90

TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC ACC AGA 507
 Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
 95 100 105

20 GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT 546
 Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn
 110 115

25 GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC 585
 Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys
 120 125 130

CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG 624
 30 Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
 135 140

GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC 663
 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
 35 145 150 155

ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC 702
Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
160 165 170

5 AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 741
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
175 180

10 AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG 780
Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
185 190 195

15 ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT 819
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
200 205

20 GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA 858
Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
210 215 220

25 GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT 897
Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
225 230 235

30 GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC 936
Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
240 245

35 ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970
Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

GAAAGACTTC ACTGTGGAAG AAATTCCCTTC CTTACCTGAA AGGTTCAGGT 1020

35 AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070

TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCC CAAAAAAA 1120

AAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1170

5 AAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 299 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
-40 -35 -30

20 Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
-25 -20 -15

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-10 -5 1 5

25 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
10 15 20

Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
25 30 35

30 Gln Gln Thr Val Ala Pro Gln Gln Arg His Ser Phe Lys Gly
40 45 50

Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
35 55 60 65

159
266 265 264 263 262 261 260

	Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn		
	70	75	80
	Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln		
5	85	90	95
	Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln		
	100	105	110
10	Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys		
	115	120	125
	Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn		
	130	135	140
159	Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala		
266	145	150	155
	Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr		
20	160	165	170
	Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr		
	175	180	185
25	Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr		
	190	195	200
	Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr		
	205	210	215
30	Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr		
	220	225	230
	Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile		
35	235	240	245

Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1180 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15 GCTGTGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTTGGGA GTTGACCAAG AG ATG CAA GGG GTG AAG GAG 90
Met Gln Gly Val Lys Glu
-40 -35

20 CGC TTC CTA CCG TTA GGG AAC TCT GGG GAC AGA GCG CCC 129
Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
-30 -25

25 CCG CCG CCT GAT GGC CGA GGC AGG GTG CGA CCC AGG ACC 168
Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
-20 -15 -10

30 CAG GAC GGC GTC GGG AAC CAT ACC ATG GCC CGG ATC CCC 207
Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-5 1 5

AAG ACC CTA AAG TTC GTC GTC GTC ATC GTC GCG GTC CTG 246
Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
35 10 15

195
200
205
210
215
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225
230
235
240
245
250

CTG CCA GTC CTA GCT TAC TCT GCC ACC ACT GCC CGG CAG 285
Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
20 25 30

5 GAG GAA GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG 324
Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln
35 40

10 AGG CAC AGC TTC AAG GGG GAG GAG TGT CCA GCA GGA TCT 363
Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
45 50 55

CAT AGA TCA GAA CAT ACT GGA GCC TGT AAC CCG TGC ACA 402
His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
195 60 65 70

GAG GGT GTG GAT TAC ACC AAC GCT TCC AAC AAT GAA CCT 441
Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
75 80

20 TCT TGC TTC CCA TGT ACA GTT TGT AAA TCA GAT CAA AAA 480
Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
85 90 95

25 CAT AAA AGT TCC TGC ACC ATG ACC AGA GAC ACA GTG TGT 519
His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
100 105

30 CAG TGT AAA GAA GGC ACC TTC CGG AAT GAA AAC TCC CCA 558
Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
110 115 120

35 GAG ATG TGC CGG AAG TGT AGC AGG TGC CCT AGT GGG GAA 597
Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
125 130 135

GTC CAA GTC AGT AAT TGT ACG TCC TGG GAT GAT ATC CAG 636
Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
140 145

5 TGT GTT GAA GAA TTT GGT GCC AAT GCC ACT GTG GAA ACC 675
Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
150 155 160

10 CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCG GGG ACT 714
Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr
165 170

150 CCT GCC CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCA 753
Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro
175 180 185

20 GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG ACC ACC 792
Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
190 195 200

AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 831
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
205 210

25 ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG 870
Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
215 220 225

30 ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC TCT TCT CAT 909
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His
230 235

35 TAC CTC TCA TGC ACC ATC GTA GGG ATC ATA GTT CTA ATT 948
Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile
240 245 250

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990
Val Leu Leu Ile Val Phe Val
255 259

5 AAATTCCCTTC CTTACCTGAA AGGTTCAGGT AGGCGCTGGC TGAGGGCGGG 1040

GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC 1090

AGAAACGCCT GCCCCTGCC CAAAAAAA AAAAAAAA AAAAAAAA 1140

10

AAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

150 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTAAAACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43

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(2) INFORMATION FOR SEQ ID NO:6:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFORMATION FOR SEQ ID NO:7:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
1 5 10 15

15 Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly
20 25 30

Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
35 40 45

20 Gly Cys Arg Lys
49

25 (2) INFORMATION FOR SEQ ID NO:8:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
1 5 10 15

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
5 35 40 45

Cys Lys Glu

48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15 GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

20 GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCCACAA AATACACCGA CGATGCCGA TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
Met Glu
1

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
10 Gln Arg Gly Gin Asn Ala Pro Ala Ala Ser Gly Ala Arg
5 10 15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
15 20 25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
20 30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
Val Ala Ala Val Leu Leu Val Ser Ala Glu Ser Ala
25 45 50

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
55 60 65

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
30 Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
70 75 80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
35 85 90

TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
95 100 105

5 TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
110 115

10 GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
120 125 130

15 AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
135 140 145

20 GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
150 155

25 GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
160 165 170

30 CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
175 180

35 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
185 190 195

GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
215 220

5 GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847
Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
225 230 235

10 GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
240 245

15 TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925
Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val
250 255 260

20 CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
265 270 275

25 CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003
Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
280 285

30 GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
290 295 300

35 GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
305 310

GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
315 320 325

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
330 335 340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
345 350

10 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
355 360 365

15 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
370 375

20 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
380 385 390

25 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

30 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAAGTGAGA 1400
Ala Asp Ser Ala Xaa Ser
410 411

CCTTCCCTGG TTTACCTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

35 AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTCACTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTCAC AGCACTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAG AAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg

1 5 10 15

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Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro

20 25 30

25

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val

35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp

50 55 60

30

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser

65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp

80 85 90

35

DRAFT

Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
95 100 105

His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
5 110 115 120

Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
125 130 135

10 Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
140 145 150

Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
155 160 165

15 Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
170 175 180

Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
20 185 190 195

Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

25 Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Asp
215 220 225

Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
30 230 235 240

Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
245 250 255

35 Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
260 265 270

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Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
5 290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
10 305 310 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
15 335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
20 365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
25 395 400 405

Ala Asp Ser Ala Xaa Ser
30 410 411

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20 AGGATGGGAA GTGTGTGATA TATCCTTGAT 30